SEQUENCE LISTING

<110> Wang, Huaming
van Gastel, Frans
Aehle, Wolfgang
Rodrigues, Ana
Topozada, Amr

<120> Phenol Oxidizing Enzyme Variants

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<141> 2000-09-07

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<213> Stachybotrys chartarum

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<210> 2
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<212> PRT
<213> Stachybotrys chartarum

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35 40 45
Ala Leu Tyr Glu Val Pro Leu Pro Ile Pro Pro Leu Lys Ala Pro Asn
50 55 60
Thr Val Pro Asn Pro Asn Thr Gly Glu Asp Ile Leu Tyr Tyr Glu Met
65 70 75 80
Glu Ile Arg Pro Phe Ser His Gln Ile Tyr Pro Asp Leu Glu Pro Ala
85 90 95
Asn Met Val Gly Tyr Asp Gly Met Ser Pro Gly Pro Thr Ile Ile Val
100 105 110
Pro Arg Gly Thr Glu Ser Val Val Arg Phe Val Asn Ser Gly Glu Asn
115 120 125
Thr Ser Pro Asn Ser Val His Leu His Gly Ser Phe Ser Arg Ala Pro
130 135 140
Phe Asp Gly Trp Ala Glu Asp Thr Thr Gln Pro Gly Glu Tyr Lys Asp
145 150 155 160
Tyr Tyr Tyr Pro Asn Arg Gln Ala Ala Arg Met Leu Trp Tyr His Asp
165 170 175
His Ala Met Ser Ile Thr Ala Glu Asn Ala Tyr Met Gly Gln Ala Gly
180 185 190
Val Tyr Met Ile Gln Asp Pro Ala Glu Asp Ala Leu Asn Leu Pro Ser
195 200 205
Gly Tyr Gly Glu Phe Asp Ile Pro Leu Val Leu Thr Ala Lys Arg Tyr
210 215 220
Asn Ala Asp Gly Thr Leu Phe Ser Thr Asn Gly Glu Val Ser Ser Phe
225 230 235 240
Trp Gly Asp Val Ile Gln Val Asn Gly Gln Pro Trp Pro Met Leu Asn
245 250 255
Val Gln Pro Arg Lys Tyr Arg Phe Arg Phe Leu Asn Ala Ala Val Ser
260 265 270
Arg Ser Phe Ala Leu Tyr Leu Ala Thr Ser Glu Asp Ser Glu Thr Arg
275 280 285
Leu Pro Phe Gln Val Ile Ala Ala Asp Gly Gly Leu Leu Glu Gly Pro
290 295 300
Val Asp Thr Asp Thr Leu Tyr Ile Ser Met Ala Glu Arg Trp Glu Val
305 310 315 320
Val Ile Asp Phe Ser Thr Phe Ala Gly Gln Ser Ile Asp Ile Arg Asn
325 330 335
Leu Pro Gly Ala Asp Gly Leu Gly Val Glu Pro Glu Phe Asp Asn Thr
340 345 350
Asp Lys Val Met Arg Phe Val Val Asp Glu Val Leu Glu Ser Pro Asp
355 360 365
Thr Ser Glu Val Pro Ala Asn Leu Arg Asp Val Pro Phe Pro Glu Gly

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    370                 375                 380
Gly Asn Trp Asp Pro Ala Asn Pro Thr Asp Asp Glu Thr Phe Thr Phe
385                 390                 395                 400
Gly Arg Ala Asn Gly Gln Trp Thr Ile Asn Gly Val Thr Phe Ser Asp
                405                 410                 415
Val Glu Asn Arg Leu Leu Arg Asn Val Pro Arg Asp Thr Val Glu Ile
            420                 425                 430
Trp Arg Leu Glu Asn Asn Ser Asn Gly Trp Thr His Pro Val His Ile
        435                 440                 445
His Leu Val Asp Phe Arg Val Leu Ser Arg Ser Thr Ala Arg Gly Val
    450                 455                 460
Glu Pro Tyr Glu Ala Ala Gly Leu Lys Asp Val Val Trp Leu Ala Arg
465                 470                 475                 480
Arg Glu Val Val Tyr Val Glu Ala His Tyr Ala Pro Phe Pro Gly Val
                485                 490                 495
Tyr Met Leu His Cys His Asn Leu Ile His Glu Asp His Asp Met Met
            500                 505                 510
Ala Ala Phe Asn Val Thr Val Leu Gly Asp Tyr Gly Tyr Asn Tyr Thr
        515                 520                 525
Glu Phe Ile Asp Pro Met Glu Pro Leu Trp Arg Pro Arg Pro Phe Leu
    530                 535                 540
Leu Gly Glu Phe Glu Asn Gly Ser Gly Asp Phe Ser Glu Leu Ala Ile
545                 550                 555                 560
Thr Asp Arg Ile Gln Glu Met Ala Ser Phe Asn Pro Tyr Ala Gln Ala
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Asp Asp Asp Ala Ala Glu Glu
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<210> 3
<211> 2095
<212> DNA
<213> Stachybotrys chartarum

<400> 3

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gatcggcggc agctctgtcg atgccagatc cgttgctggt cgatcgacag acatgccttc     180
cggtctcacc aagaggcaga cgcagctgag tcctcccctg gccttgtacg aagtgcctct     240
gccgatccct cctctgaagg cgcccaagta gtaagtacat tctataggct agcagagcca     300
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tgaggtgcct gccaacctcc gagatgttcc tttccccgag ggcggcaact gggaccccgc    1380
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tgagatctgg cgacttgaga acaactccaa cggttggact caccctgttc acattcacct    1560
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gctgctttca atgtcactgt tctcggtgac tatggctaca actacaccga gttcattgac    1860
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tacgcccagg ctgatgatga tgccgctgag gagtaaatat gatgatcgtc gaatgattta    2040
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<213> Myrothecium verucaria

<400> 4

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Gly His Leu Phe Lys Arg Val Ala Gln Ile Ser Pro Gln Tyr Pro Met
        35                  40                  45
Phe Thr Val Pro Leu Pro Ile Pro Pro Val Lys Gln Pro Arg Leu Thr
    50                  55                  60
Val Thr Asn Pro Val Asn Gly Gln Glu Ile Trp Tyr Tyr Glu Val Glu
65                  70                  75                  80
Ile Lys Pro Phe Thr His Gln Val Tyr Pro Asp Leu Gly Ser Ala Asp
                85                  90                  95
Leu Val Gly Tyr Asp Gly Met Ser Pro Gly Pro Thr Phe Gln Val Pro
            100                 105                 110
Arg Gly Val Glu Thr Val Val Arg Phe Ile Asn Asn Ala Glu Ala Pro
        115                 120                 125
Asn Ser Val His Leu His Gly Ser Phe Ser Arg Ala Ala Phe Asp Gly
    130                 135                 140
Trp Ala Glu Asp Ile Thr Glu Pro Gly Ser Phe Lys Asp Tyr Tyr Tyr
145                 150                 155                 160
Pro Asn Arg Gln Ser Ala Arg Thr Leu Trp Tyr His Asp His Ala Met
                165                 170                 175
His Ile Thr Ala Glu Asn Ala Tyr Arg Gly Gln Ala Gly Leu Tyr Met
            180                 185                 190
Leu Thr Asp Pro Ala Glu Asp Ala Leu Asn Leu Pro Ser Gly Tyr Gly
        195                 200                 205
Glu Phe Asp Ile Pro Met Ile Leu Thr Ser Lys Gln Tyr Thr Ala Asn
    210                 215                 220
Gly Asn Leu Val Thr Thr Asn Gly Glu Leu Asn Ser Phe Trp Gly Asp
225                 230                 235                 240
Val Ile His Val Asn Gly Gln Pro Trp Pro Phe Lys Asn Val Glu Pro
                245                 250                 255
Arg Lys Tyr Arg Phe Arg Phe Leu Asp Ala Ala Val Ser Arg Ser Phe
            260                 265                 270
Gly Leu Tyr Phe Ala Asp Thr Asp Ala Ile Asp Thr Arg Leu Pro Phe
        275                 280                 285
Lys Val Ile Ala Ser Asp Ser Gly Leu Leu Glu His Pro Ala Asp Thr
    290                 295                 300
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Ser Leu Leu Tyr Ile Ser Met Ala Glu Arg Tyr Glu Val Val Phe Asp
305                 310                 315                 320
Phe Ser Asp Tyr Ala Gly Lys Thr Ile Glu Leu Arg Asn Leu Gly Gly
                325                 330                 335
Ser Ile Gly Gly Ile Gly Thr Asp Thr Asp Tyr Asp Asn Thr Asp Lys
            340                 345                 350
Val Met Arg Phe Val Val Ala Asp Asp Thr Thr Gln Pro Asp Thr Ser
        355                 360                 365
Val Val Pro Ala Asn Leu Arg Asp Val Pro Phe Pro Ser Pro Thr Thr
    370                 375                 380
Asn Thr Pro Arg Gln Phe Arg Phe Gly Arg Thr Gly Pro Thr Trp Thr
385                 390                 395                 400
Ile Asn Gly Val Ala Phe Ala Asp Val Gln Asn Arg Leu Leu Ala Asn
                405                 410                 415
Val Pro Val Gly Thr Val Glu Arg Trp Glu Leu Ile Asn Ala Gly Asn
            420                 425                 430
Gly Trp Thr His Pro Ile His Ile His Leu Val Asp Phe Lys Val Ile
        435                 440                 445
Ser Arg Thr Ser Gly Asn Asn Ala Arg Thr Val Met Pro Tyr Glu Ser
    450                 455                 460
Gly Leu Lys Asp Val Val Trp Leu Gly Arg Arg Glu Thr Val Val Val
465                 470                 475                 480
Glu Ala His Tyr Ala Pro Phe Pro Gly Val Tyr Met Phe His Cys His
                485                 490                 495
Asn Leu Ile His Glu Asp His Asp Met Met Ala Ala Phe Asn Ala Thr
            500                 505                 510
Val Leu Pro Asp Tyr Gly Tyr Asn Ala Thr Val Phe Val Asp Pro Met
        515                 520                 525
Glu Glu Leu Trp Gln Ala Arg Pro Tyr Glu Leu Gly Glu Phe Gln Ala
    530                 535                 540
Gln Ser Gly Gln Phe Ser Val Gln Ala Val Thr Glu Arg Ile Gln Thr
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Met Ala Glu Tyr Arg Pro Tyr Ala Ala Ala Asp Glu
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<210> 5
<211> 21
<212> PRT
<213> Stachybotrys chartarum

<400> 5

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Gly Ser Phe Ser Arg
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<210> 6
<211> 18
<212> PRT
<213> Stachybotrys chartarum

<400> 6

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Ala Arg
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<211> 20
<212> DNA
<213> Artificial Sequence

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<210> 8
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